

Percolation with Multiple Giant Clusters

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We study the evolution of percolation with freezing. Specifically, we consider cluster formation via two competing processes: irreversible aggregation and freezing. We find that when the freezing rate exceeds a certain threshold, the percolation transition is suppressed. Below this threshold, the system undergoes a series of percolation transitions with multiple giant clusters (“gels”) formed. Giant clusters are not self-averaging as their total number and their sizes fluctuate from realization to realization. The size distribution F_k , of frozen clusters of size k , has a universal tail, $F_k \sim k^{-3}$. We propose freezing as a practical mechanism for controlling the gel size.

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Percolation was originally discovered in the context of polymerization and gelation [1, 2]. Percolation has found numerous applications in physics [3, 4], geophysics [5], chemistry [6], and biology [7]. It plays an important role in a vast array of natural and artificial processes ranging from flow in porous media [8] and cloud formation [9, 10] to evolution of random graphs [11, 12], combinatorial optimization [13], algorithmic complexity [14], amorphous computing, and DNA computing using self-assembly [15].

We study the evolution of percolation using the framework of aggregation. An aggregation process typically begins with a huge number of molecular units (“monomers”) that join irreversibly to form clusters (“polymers”). At some time, a giant cluster (“gel”) containing a finite fraction of the monomers in the system is born, and it grows to engulf the entire system. In this classic percolation picture only a single gel forms, but in many natural and artificial processes the system freezes into a non-trivial final state with multiple gels or even micro-gels [16, 17]. In this Letter, we show that aggregation with freezing naturally lead to formation of multiple gels and that freezing is also a convenient mechanism for controlling the gel size.

We analyze the simplest aggregation with freezing process where there are two types of clusters: active and frozen. Active clusters join by binary aggregation into larger active clusters. The aggregation rate is proportional to the product of the two cluster sizes [9, 18, 19]; this is equivalent to the gelation model of Flory and Stockmayer where a chemical bond between two monomers joins their respective polymers [1, 2]. In parallel, active clusters may become frozen at a size-independent constant rate α . These frozen clusters are passive, that is they do not interact with other (active or passive) clusters.

This process is conveniently studied using the rate equation approach. The density $c_k(t)$ of active clusters of mass k at time t (that is, made up from k monomers)

satisfies

$$\frac{dc_k}{dt} = \frac{1}{2} \sum_{i+j=k} (ic_i)(jc_j) - mkc_k - \alpha c_k, \quad (1)$$

with $m(t)$ the mass density of active clusters. The first two terms on the right-hand side describe how the cluster size distribution changes due to aggregation, and the last term accounts for loss due to freezing. The quantity $m(t)$ is subtle. Generally, it equals the mass density of all active clusters including possibly giant clusters, but when there are no giant clusters, i.e., all clusters are finite in size, then $m(t) \equiv M_1(t)$ with the moments defined via $M_n(t) \equiv \langle k^n \rangle = \sum_{k \geq 1} k^n c_k(t)$. We are interested in the evolution starting with finite clusters only.

The gelation transition. Initially, all clusters are finite in size, so $m = M_1$. The moments M_n provide a useful probe of the dynamics. From the governing equation (1), the second moment of the size distribution M_2 obeys the closed equation $dM_2/dt = M_2(M_2 - \alpha)$. For arbitrary initial condition,

$$M_2(t) = \alpha \left[\left(\frac{\alpha}{\alpha_c} - 1 \right) e^{\alpha t} + 1 \right]^{-1}. \quad (2)$$

There is a critical freezing rate $\alpha_c = M_2(0)$. For fast freezing, $\alpha \geq \alpha_c$, the second moment is always finite indicating that clusters remain finite at all times. In this case, there is no gelation. For slow freezing, $\alpha < \alpha_c$, there is a finite time singularity indicating that an infinite cluster, the gel, emerges in a finite time [20]. The gelation time is

$$t_g = -\frac{1}{\alpha} \ln \left(1 - \frac{\alpha}{\alpha_c} \right). \quad (3)$$

The gelation point marks two phases. Prior to the gelation point, the system contains only finite clusters that undergo cluster-cluster aggregation (“coagulation phase”). Past the gelation point, the gel grows via

cluster-gel aggregation (“gelation phase”). We analyze these two phases in order.

Coagulation phase. Coagulation occurs for $\alpha \geq \alpha_c$ at all times or for $\alpha < \alpha_c$ when $t < t_g$. From (1), the mass density of active clusters satisfies $dm/dt = -\alpha m$, and thus, ordinary exponential decay occurs,

$$m(t) = m(0)e^{-\alpha t}. \quad (4)$$

For concreteness, we consider the monodisperse initial conditions $c_k(0) = \delta_{k,1}$. In this case $M_n(0) = 1$ and consequently, $\alpha_c = 1$. The cluster size distribution is obtained using the transformed distribution, $c_k = e^{-\alpha t} C_k$, and the modified time variable

$$\tau = \int_0^t dt' e^{-\alpha t'} = \frac{1 - e^{-\alpha t}}{\alpha} \quad (5)$$

that increases monotonically with the physical time and reaches $\tau \rightarrow 1/\alpha$ as $t \rightarrow \infty$. With these transformations, Eq. (1) reduces to the no-freezing case

$$\frac{dC_k}{d\tau} = \frac{1}{2} \sum_{i+j=k} (iC_i)(jC_j) - kC_k. \quad (6)$$

From the well-known solution of this equation [21, 22], the cluster-size distribution is

$$c_k(t) = \frac{k^{k-2}}{k!} \tau^{k-1} e^{-k\tau - \alpha t}. \quad (7)$$

Generally, the size distribution decays exponentially at large sizes and the typical cluster size is finite. The gelation time (3) is simply $\tau_g = 1$. Of course, no gelation occurs when $\alpha > 1$ because $\tau < 1/\alpha < 1$. Otherwise, as the gelation point is approached, $t \rightarrow t_g$, the characteristic cluster size diverges $k \sim (t_g - t)^{-2}$. The gelation point is marked by an algebraic divergence of the size distribution $c_k \sim (1 - \alpha)k^{-5/2}$ for large k . We note that the mass density decreases linearly with the modified time, $m = 1 - \alpha\tau$, and that at the gelation point, the mass is simply $m(\tau_g) = 1 - \alpha$.

Gelation phase. Past the gelation transition, a giant cluster containing a finite fraction of the mass in the system forms. In addition to cluster-cluster aggregation, cluster-gel aggregation takes place with the giant cluster growing at the expense of finite clusters. In parallel, all clusters may undergo freezing and particularly, the gel itself may freeze.

Formally, the size distribution (7) generalizes to

$$c_k(t) = \frac{k^{k-2}}{k!} \tau^{k-1} e^{-ku - \alpha t} \quad (8)$$

with $u(t) = \int_0^t dt' m(t')$. Statistical properties of the size distribution are derived from the generating function $c(z, t) = \sum_{k \geq 1} kc_k(t)e^{kz}$ that equals

$$c(z, t) = \tau^{-1} e^{-\alpha t} G(z + \ln \tau - u) \quad (9)$$

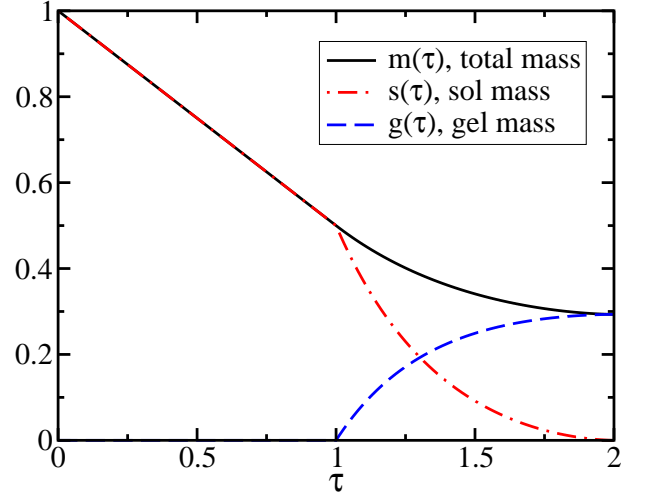


FIG. 1: The total mass, the sol mass, and the gel mass versus modified time τ for $\alpha = 1/2$. These curves hold as long as the gel remains active.

where $G(z) = \sum_{k \geq 1} \frac{k^{k-1}}{k!} e^{kz}$ is the “tree” function [23].

During the gelation phase, active clusters consist of finite clusters, the “sol”, with mass s , and the gel with mass g . The total mass density of clusters, $m = s + g$, decays according to

$$\frac{dm}{dt} = -\alpha s. \quad (10)$$

The sol mass decays according to $ds/dt = -gM_2 - \alpha s$ obtained from (1) using $s = M_1$. The first two moments follow from the generating function, $M_1 = c(0)$ and $M_2 = c'(0)$, and using the identity $G'(z) = G/(1 - G)$ [24], yields $M_2 = s/(1 - s\tau e^{\alpha t})$. The evolution equation for the sol mass becomes explicit,

$$\frac{ds}{dt} = -\frac{s(m - s)}{1 - s\tau e^{\alpha t}} - \alpha s. \quad (11)$$

Equations (10) and (11) are subject to the initial conditions $m(t_g) = s(t_g) = 1 - \alpha$. Once the masses are found, the formal solution (8) becomes explicit. Results of numerical integration of Eqs. (10) and (11) are shown on Fig. 1. In the vicinity of the gelation transition, the gel mass grows linearly with time:

$$g(t) \simeq 2(1 - \alpha)^2 (t - t_g) \quad (12)$$

as $t \downarrow t_g$. The quadratic dependence on the freezing rate implies that the emerging gel is very small when $\alpha \uparrow \alpha_c$. Thus, micro-gels, that may be practically indistinguishable from large clusters, emerge. Moreover, the maximal gel size must be smaller than $1 - \alpha$. We conclude that freezing can be used to control the gel size, as gels of arbitrarily small size can be produced using freezing rates just below criticality.

Multiple giant clusters. At any time during the gelation phase, the gel itself may freeze. This freezing process

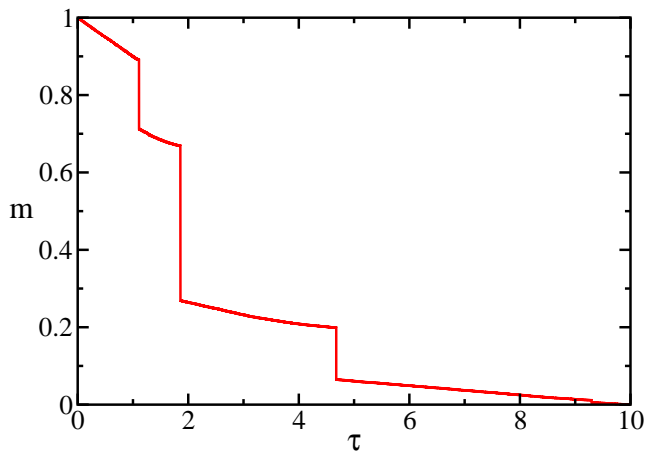


FIG. 2: The mass density m versus time τ . Shown are results of a Monte Carlo simulation with system size $N = 10^5$ and freezing rate $\alpha = 0.1$. The system alternates between the coagulation phase and the gelation phase. In the former phase the mass decreases linearly according to (4) such that depletion occurs at time $\tau = 1/\alpha$. In the latter phase, the active mass decreases slower than linear according to (10) and (11). The gelation phase ends when the gel freezes.

is random: the gel lifetime T is a random variable that is exponentially distributed, $P(T) = \alpha e^{-\alpha T}$. Until the gel freezes, the system evolves deterministically, so the mass of the frozen gel is $g(t_g + T)$. When the gel freezes, the total active mass $m(t)$ is discontinuous: it exhibits a downward jump (Fig. 2). Given that the duration of the gelation phase is governed by a random process, the mass of the frozen gel is also random. It fluctuates from realization to realization, i.e., it is not a self-averaging quantity.

When the gel freezes, the system re-enters the coagulation phase because all remaining clusters are finite. The initial conditions are dictated by the duration of the preceding gelation phase and are therefore also stochastic. Nevertheless, once the initial state is set, the evolution in the coagulation phase is deterministic. The gel is frozen so it no longer affects the evolution and only cluster-cluster aggregation occurs. Let us assume that the gel freezes at time t_f . Resetting time to zero, the first and the second moments are simply given by Eqs. (4) and (2), respectively, with $M_n(0)$ replaced by $M_n(t_f)$. Note that $M_n(t_f)$ contains contributions from *finite* clusters only. A second gelation occurs if the freezing rate is sufficiently small, $\alpha < M_2(t_f)$. Otherwise, the system forever remains in the coagulation phase.

Cyclic dynamics. The general picture is now clear: the process starts and ends in coagulation and throughout the evolution, the system alternates between coagulation and gelation. Once the initial conditions are set, the behavior throughout the coagulation phase and throughout the gelation phase are both deterministic. Each gelation phase ends with freezing of the active gel. Since the dura-

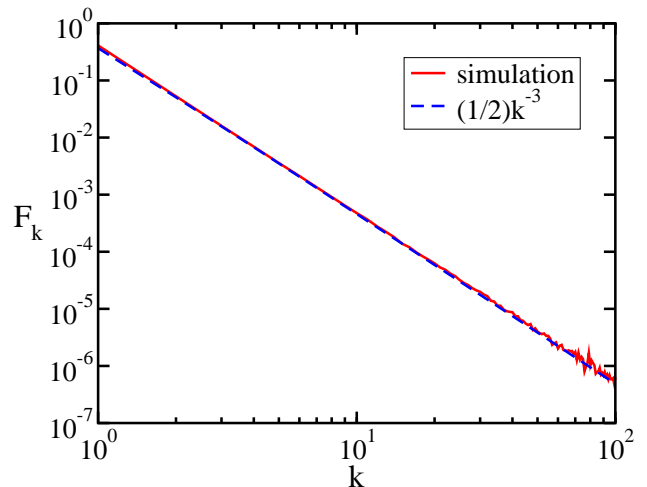


FIG. 3: The size distribution of the frozen clusters for $\alpha = 1/2$. The simulation results represent an average over 10^2 independent realizations in a system of size $N = 10^6$.

tion of the gelation phase is random, the size of the giant clusters, and their number are both random variables. Generically, the system exhibits a series of percolation transitions, each producing a frozen gel, so that overall, multiple gels are produced. The random freezing process governs the number of percolation transitions as well as the size of the frozen gels.

The magnitude of the second moment when the gel freezes determines whether a successive gelation occurs. Because the second moment diverges at the gelation point, there is a time window past the gelation time where the second moment exceeds the freezing rate. If the gel freezes during this window, another percolation transition is bound to occur. Therefore, the maximal number of frozen gels is unbounded.

Monte Carlo simulations confirm this picture (Fig. 2). In the simulations, we keep track the total aggregation rate $R_a = N(M_1^2 - M_2)/2$ and the total freezing rate $R_f = \alpha N M_0$. Aggregation occurs with probability $R_a/(R_a + R_f)$, and freezing occurs with the complementary probability. A cluster is chosen for aggregation with probability proportional to its size. Time is augmented by $\Delta t = 1/(R_a + R_f)$ after each aggregation or freezing event.

Frozen clusters. We now turn to the frozen clusters. Their density is found from $dF_k/dt = \alpha c_k$. When $\alpha \geq \alpha_c$, the density of active clusters over the entire time range is given by Eq. (7), and therefore $F_k(t)$ is found by simple integration. In particular, the final density is

$$F_k(\infty) = \frac{\alpha}{k^2 \cdot k!} \gamma(k, k/\alpha) \quad (13)$$

where $\gamma(n, x) = \int_0^x dy y^{n-1} e^{-y}$ is the incomplete gamma function. At large sizes, the size distribution of frozen

clusters decays according to

$$F_k(\infty) \simeq \begin{cases} \frac{1}{2} \cdot k^{-3} & \alpha = 1 \\ A(\alpha) k^{-7/2} \exp[-B(\alpha)k] & \alpha > 1 \end{cases} \quad (14)$$

where $A = (2\pi)^{-1/2} \alpha^2 / (\alpha - 1)$ and $B = \alpha^{-1} + \ln \alpha - 1$.

Similarly, we may obtain the density of frozen clusters formed in the first coagulation case. Integrating (7) gives $F_k(t_g) = \frac{\alpha}{k^2 \cdot k!} \gamma(k, k)$. This size distribution decays algebraically, $F_k(t_g) \simeq \frac{\alpha}{2} k^{-3}$. However, enumerating the frozen clusters that are born past the first gelation point is more complicated since the deterministic patches are punctuated by random jumps. In fact, even the total mass of frozen clusters becomes a random quantity because it is a complementary quantity to the final mass density of frozen gels. Interestingly, numerical simulations suggest that the tail behavior

$$F_k \simeq D k^{-3} \quad (15)$$

is universal (Fig. 3). Even the prefactor D appears to depend only weakly upon the freezing rate α . This shows that the final distribution of frozen clusters is dominated by the coagulation phase. Indeed, in each such phase, the tail behavior is k^{-3} , and furthermore, in the gelation phase, large clusters are more likely to be consumed by the gel. These results suggest that freezing leads to an additional non-trivial critical exponent $\gamma = 3$.

In conclusion, we have found that freezing leads to multiple percolation transitions. The system evolves in a cyclic fashion alternating between coagulation and gelation. Depending on the freezing rate, the system may form no gels, a single gel, or multiple gels. Most statistical characteristics are non-self-averaging because they are controlled by the random freezing of gels.

Freezing provides a practical mechanism for controlling gelation. It may be used to engineer micro-gels of desired size by implementing variable cooling rates. Slow freezing followed by rapid freezing can be used to produce gels of prescribed size, while near-critical freezing produces micro-gels of arbitrarily small size.

There are a number of interesting potential generalizations of the present work. The most natural is percolation in finite dimensions. Percolation is analytically tractable only in two dimensions, though even in that situation it is not clear how to derive the exponent characterizing the tail of the final distribution of frozen clusters. One may also consider situations with different freezing mechanisms [25], particularly for finite and infinite clusters. We also solved for the case where infinite clusters freeze immediately [26]. In this case, there is no breakdown of self-averaging and the final density of frozen clusters mimics the critical behavior of active clusters, $\gamma = 5/2$.

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